



CDS: SPBC16G5.09



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General Information

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Systematic Name SPBC16G5.09
 Status role inferred from homology
 Product serine carboxypeptidase (predicted)
 Type CDS
 Sequence DNA and Protein

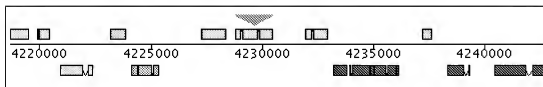
Location

Chromosome 2
 Contig Location 4228817..4230463 (Unspliced length: 1647 bp)
 Exons join(4228817..4229044 , 4229112..4229810 , 4229858..4230463) (Spliced length: 1533 bp)

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Context Map:



SPBC16G5.03 mrp123 SPBC16G5.05c SPBC16G5.06 SPBC16G5.07c trp4 >SPBC16G5.09< SPBC16G5.10
 bag101 top3 SPBC16G5.13 rps3 flk2

Curation

Term
 peptidase family S10
 predicted N-terminal signal sequence
 similar to *S. cerevisiae* YGL203C
 conserved family

Other genes annotated to this term
 (1 Other)
 (254 Others)
 (0 Others)
 (54 Others)

Predicted Peptide Properties

Mass	57.6 kDa	Amino acids	510
Isoelectric point	pH 4.5	Charge	-24.5

Signal Peptide predicted for SPBC16G5.09 by SignalP 2.0 HMM (Signal peptide probability 0.961, signal anchor probability 0.003) with cleavage site probability 0.864 between residues 21 and 22

Transmembrane

Domains	1 probable transmembrane helix predicted for SPBC16G5.09 by TMHMM2.0 at aa 469-491
GPI Anchor	Not found

Gene Ontology Annotation

Term (browse Amigo)	Qualifier Evidence	Other genes annotated to this term
Biological Process		
proteolysis	IEA (GOA:interproGO_REF:0000002) with InterPro:IPR001563	228 others
Cellular Component		
integral to membrane	IEA (GOA:spkwGO_REF:0000004) with SP_KW:KW-0812	793 others
trans-Golgi network vacuole	ISS (PMID:17072883) with SGD:S000003171	2 others
Molecular Function		
carboxypeptidase D activity	ISS (PMID:17072883) with SGD:S000003171	none

Catalytic Activity

EC 3.4.16.6 : [IUBMB](#)

Published Expression Profiles

Gene Expression Viewer [Cell Cycle](#) [Meiosis](#) [Environmental Stress](#) [Pheromone Response/Mating](#)

TranscriptomeViewer [SPBC16G5.09](#) High-resolution view of transcripts in neighbourhood

Literature

[Search for in PubMed](#)

Domain Information

[View Pfam domain structure for this gene product](#)[View SCOP superfamily](#)

DB	Accs	Description
Pfam	PF00450	Serine carboxypeptidase
MEROPS	S10.007	MEROPS
InterPro	IPR001563	Peptidase S10, serine carboxypeptidase
PRINTS	PR00724	Carboxypeptidase C serine protease (S10) family signature
ProDom	PD001189	ProDom

Database Cross-References

DB	Accs	Description
UniProtKB	Q60123	Carboxypeptidase kex1 precursor (EC 3.4.16.6) (Carboxypeptidase D).
EMBL	CU329671	Schizosaccharomyces pombe chromosome II
Biotwiki	SPBC16G5.09	Biotwiki
NCBI Entrez Gene	SPBC16G5.09	NCBI Entrez Gene
FYSSION	SPBC16G5.09	FYSSION
GermOnline	SPBC16G5.09	GermOnline
NBRP	SPBC16G5.09	Fission yeast strain database, National BioResource Project (Japan)
PIR	T39601	PIR
YOGY	SPBC16G5.09	Retrieval of eukaryotic orthologs

UniProtKB Annotation For This Protein

Catalytic Activity	Preferential release of a C-terminal arginine or lysine residue.
Function	Protease with a carboxypeptidase B-like function involved in killer toxin and alpha-factor precursor processing (By similarity).
Similarity	Belongs to the peptidase S10 family.
Subcellular Location	Vacuole membrane; Single-pass type I membrane protein.
Keywords	Carboxypeptidase (5 others), Complete proteome (4982 others), Glycoprotein (169 others), Hydrolase (451 others), Membrane (801 others), Protease (90 others), Signal (136 others), Transmembrane (651 others), Vacuole (42 others)

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